

**In the Specification**

Please amend the paragraph bridging page 7, lines 7-28 to read as follows:

“In the context of the present invention, the “bait” protein is a C-terminal portion of hairless protein of mouse (HRt) having amino acid residues 490 to 1182 (provided as SEQ ID NO:17, the nucleic acid sequence encoding amino acids 490 to 1182 is provided as SEQ ID NO:18 “Structure and Expression of the Hairless Gene of Mice,” Begona, M., *et al.*, *J. Proc. Natl. Acad. Sci, USA* 91:7717-7721, 1994) (GenBank accession no. Z32675). HR protein (aa residues 490 to 1182) contains the zinc finger domain (595-620) and three PEST domains previously identified to be potentially important for HR function. To reiterate, mouse HR very similar to human HR. Indeed, PEST sequences are often used to serve as signals for rapid protein degradation. The signals may be constitutive or conditional. The PEST-FIND computer program has been developed by M. Rechsteiner and S. W. Rogers (*PEST sequences and regulation by proteolysis, TIBS* 21, July 1996) to objectively determine whether a protein contains a PEST region. The associated algorithm, available in PC/GENE (OMIGA), defines a PEST sequence as a hydrophilic stretch of 12 or more aa residues containing at least one of each of P, E/D, and S/T in any order. PEST sequences must further be flanked by basic aa residues K, A or H, but basic residues are disallowed in the PEST sequence. PEST-FIND produces a score ranging from about +50 to –50. For classification purposes, a score of less than zero denotes a possible PEST region, but a score of greater than +5 denotes a high potential of the existence of a PEST region. For example, PEST Domains were located in the following regions of the HR protein (aa residues 490 to 1182): PEST Domain 12.26 between aa residues 522 and 546; PEST Domain 7.56 between aa residues 709 and 722; and PEST Domain 21.71 between aa residues 729 and 744.”